

RAW SEQUENCE LISTING

EFS

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Application Serial Number: 10/576,778

Source: 1FWO

Date Processed by STIC: 3/6/07

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IFWO

RAW SEQUENCE LISTING

DATE: 03/06/2007

PATENT APPLICATION: US/10/576,778

TIME: 11:18:57

Input Set : N:\efs\03_06_07\10576778_efs\Sequence_Listing.txt

Output Set: N:\CRF4\03062007\J576778.raw

3 <110> APPLICANT: Ruiz Caston, Jose et al.

5 <120> TITLE OF INVENTION: PROCESS FOR PRODUCING IN YEASTS EMPTY VIRAL CAPSIDS
CONSISTING OF

6 PROTEINS DERIVED FROM PVP2 OF THE INFECTIOUS BURSAL DISEASE

7 VIRUS (IBDV)

9 <130> FILE REFERENCE: 7572-74819

11 <140> CURRENT APPLICATION NUMBER: US 10/576,778

12 <141> CURRENT FILING DATE: 2006-04-21

14 <150> PRIOR APPLICATION NUMBER: PCT/ES2005/070052

15 <151> PRIOR FILING DATE: 2005-04-27

17 <150> PRIOR APPLICATION NUMBER: P200401044

18 <151> PRIOR FILING DATE: 2004-04-30

20 <160> NUMBER OF SEQ ID NOS: 11

22 <170> SOFTWARE: PatentIn version 3.3

24 <210> SEQ ID NO: 1

25 <211> LENGTH: 7929

26 <212> TYPE: DNA

27 <213> ORGANISM: Artificial

29 <220> FEATURE:

30 <223> OTHER INFORMATION: Nucleotide sequence of plasmid pESCURAinv/pVP2-456

33 <220> FEATURE:

34 <221> NAME/KEY: promoter

35 <222> LOCATION: (1)..(342)

36 <223> OTHER INFORMATION: Promotor Gall

38 <220> FEATURE:

39 <221> NAME/KEY: CDS

40 <222> LOCATION: (351)..(1721)

42 <400> SEQUENCE: 1

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47	tgataatgcg attagttttt tagccttatt tctggggtaa ttaatcagcg aagcgatgat	180
49	ttttgatcta ttaacagata tataaatgca aaaactgcat aaccacttta actaatactt	240
51	tcaacatttt cggtttgtat tacttcttat tcaaatgtaa taaaagtatc aacaaaaaat	300
53	tgttaatata cctctatact ttaacgtcaa ggagaaaaaa ccccggatct atg aca	356
54		Met Thr
55		1
57	aac ctg tca gat caa acc cag cag att gtt ccg ttc ata cgg agc ctt	404
58	Asn Leu Ser Asp Gln Thr Gln Gln Ile Val Pro Phe Ile Arg Ser Leu	.
59	5 10 15	
61	ctg atg cca aca acc gga ccg gcg tcc att ccg gac gac acc ctg gag	452
62	Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro Asp Asp Thr Leu Glu	
63	20 25 30	
65	aag cac act ctc agg tca gag acc tcg acc tac aat ttg act gtg ggg	500
66	Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr Val Gly	

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71					55					60					65		
73	att	gtg	ggt	gct	cac	tac	aca	ctg	cag	ggc	aat	ggg	aac	tac	aag	ttc	596
74	Ile	Val	Gly	Ala	His	Tyr	Thr	Leu	Gln	Gly	Asn	Gly	Asn	Tyr	Lys	Phe	
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77	gat	cag	atg	ctc	ctg	act	gcc	cag	aac	cta	ccg	gcc	agt	tac	aac	tac	644
78	Asp	Gln	Met	Leu	Leu	Thr	Ala	Gln	Asn	Leu	Pro	Ala	Ser	Tyr	Asn	Tyr	
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82	Cys	Arg	Leu	Val	Ser	Arg	Ser	Leu	Thr	Val	Arg	Ser	Ser	Thr	Leu	Pro	
83		100							105						110		
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90	Gly	Ser	Leu	Ser	Glu	Leu	Thr	Asp	Val	Ser	Tyr	Asn	Gly	Leu	Met	Ser	
91					135					140					145		
93	gca	aca	gcc	aac	atc	aac	gac	aaa	att	ggg	aac	gtc	cta	gta	ggg	gaa	836
94	Ala	Thr	Ala	Asn	Ile	Asn	Asp	Lys	Ile	Gly	Asn	Val	Leu	Val	Gly	Glu	
95					150					155					160		
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110	Ala	Asp	Asp	Tyr	Gln	Phe	Ser	Ser	Gln	Tyr	Gln	Pro	Gly	Gly	Val	Thr	
111					215					220					225		
113	atc	aca	ctg	ttc	tca	gcc	aac	att	gat	gcc	atc	aca	agc	ctc	agc	gtt	1076
114	Ile	Thr	Leu	Phe	Ser	Ala	Asn	Ile	Asp	Ala	Ile	Thr	Ser	Leu	Ser	Val	
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123					260					265					270		
125	gct	gtg	gcc	gca	aac	aat	ggg	ctg	acg	acc	ggc	acc	gac	aac	ctt	atg	1220
126	Ala	Val	Ala	Ala	Asn	Asn	Gly	Leu	Thr	Thr	Gly	Thr	Asp	Asn	Leu	Met	
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137 gat cag atg tca tgg tcg gca aga ggg agc cta gca gtg acg atc cat      1364
138 Asp Gln Met Ser Trp Ser Ala Arg Gly Ser Leu Ala Val Thr Ile His
139          325          330          335
141 ggt ggc aac tat cca ggg gcc ctc cgt ccc gtc acg cta gtg gcc tac      1412
142 Gly Gly Asn Tyr Pro Gly Ala Leu Arg Pro Val Thr Leu Val Ala Tyr
143          340          345          350
145 gaa aga gtg gca aca gga tcc gtc gtt acg gtc gct ggg gtg agc aac      1460
146 Glu Arg Val Ala Thr Gly Ser Val Val Thr Val Ala Gly Val Ser Asn
147 355          360          365          370
149 ttc gag ctg atc cca aat cct gaa cta gca aag aac ctg gtt aca gaa      1508
150 Phe Glu Leu Ile Pro Asn Pro Glu Leu Ala Lys Asn Leu Val Thr Glu
151          375          380          385
153 tac ggc cga ttt gac cca gga gcc atg aac tac aca aaa ttg ata ctg      1556
154 Tyr Gly Arg Phe Asp Pro Gly Ala Met Asn Tyr Thr Lys Leu Ile Leu
155          390          395          400
157 agt gag agg gac cgt ctt ggc atc aag acc gtc tgg cca aca agg gag      1604
158 Ser Glu Arg Asp Arg Leu Gly Ile Lys Thr Val Trp Pro Thr Arg Glu
159          405          410          415
161 tac act gac ttt cgt gaa tac ttc atg gag gtg gcc gac ctc aac tct      1652
162 Tyr Thr Asp Phe Arg Glu Tyr Phe Met Glu Val Ala Asp Leu Asn Ser
163          420          425          430
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170 Ile Arg Arg Ile Ala Val
171          455
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380 <210> SEQ ID NO: 2

381 <211> LENGTH: 35

382 <212> TYPE: DNA

383 <213> ORGANISM: Artificial

385 <220> FEATURE:

386 <223> OTHER INFORMATION: Oligo I, direct oligonucleotide primer used for generating

the

387 DNA fragment encoding pVP2-456 protein in combination with SEQ ID

388 NO: 3

390 <400> SEQUENCE: 2

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35

394 <210> SEQ ID NO: 3

395 <211> LENGTH: 32

396 <212> TYPE: DNA

397 <213> ORGANISM: Artificial

RAW SEQUENCE LISTING ERROR SUMMARY

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Input Set : N:\efs\03_06_07\10576778_efs\Sequence_Listing.txt

Output Set: N:\CRF4\03062007\J576778.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,9,10,11

VERIFICATION SUMMARY

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